



SEQUENCE LISTING

1) GENERAL INFORMATION:

(i) APPLICANT: Charo, Israel
Coughlin, Shaun

(ii) TITLE OF INVENTION: MAMMALIAN MONOCYTE CHEMOATTRACTANT
PROTEIN RECEPTORS

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/446,669
(B) FILING DATE: May 25, 1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Neeley, Richard
(B) REGISTRATION NUMBER: 30,092
(C) REFERENCE/DOCKET NUMBER: UCAL-237/01US

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 40..1161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATTGAACA AGGACGCATT TCCCCAGTAC ATCCACAAC ATG CTG TCC ACA TCT	54
Met Leu Ser Thr Ser	
1 5	
CGT TCT CGG TTT ATC AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC	102
Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr	
10 15 20	
ACC TTT TTT GAT TAT GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG	150
Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val	
25 30 35	
AAG CAA ATT GGG GCC CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC	198
Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe	
40 45 50	
ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC	246
Ile Phe Gly Phe Val Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn	
55 60 65	
TGC AAA AAG CTG AAG TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC	294
Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala	
70 75 80 85	
ATC TCT GAT CTG CTT TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT	342
Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser	
90 95 100	

GCT GCA AAT GAG TGG GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA	390
Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr	
105 110 115	
GGG CTG TAT CAC ATC GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC	438
Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu	
120 125 130	
CTG ACA ATC GAT AGA TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA	486
Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu	
135 140 145	
AAA GCC AGG ACG GTC ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG	534
Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp	
150 155 160 165	
TTG GTG GCT GTG TTT GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC	582
Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys	
170 175 180	
CAG AAA GAA GAT TCT GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA	630
Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly	
185 190 195	
TGG AAT AAT TTC CAC ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG	678
Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu	
200 205 210	
CCG CTG CTC ATC ATG GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG	726
Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu	
215 220 225	
CTT CGG TGT CGA AAC GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC	774
Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Val Ile	
230 235 240 245	
TTC ACC ATC ATG ATT GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT	822
Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile	
250 255 260	
GTC ATT CTC CTG AAC ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT	870
Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys	
265 270 275	
GAA AGC ACC AGT CAA CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT	918
Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu	
280 285 290	

GGG ATG ACT CAC TGC TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG	966
Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly	
295 300 305	
GAG AAG TTC AGA AGC CTT TTT CAC ATA GCT CTT GGC TGT AGG ATT GCC	1014
Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu Gly Cys Arg Ile Ala	
310 315 320 325	
CCA CTC CAA AAA CCA GTG TGT GGA GGT CCA GGA GTG AGA CCA GGA AAG	1062
Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly Val Arg Pro Gly Lys	
330 335 340	
AAT GTG AAA GTG ACT ACA CAA GGA CTC CTC GAT GGT CGT GGA AAA GGA	1110
Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp Gly Arg Gly Lys Gly	
345 350 355	
AAG TCA ATT GGC AGA GCC CCT GAA GCC AGT CTT CAG GAC AAA GAA GGA	1158
Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu Gln Asp Lys Glu Gly	
360 365 370	
GCC TAGAGACAGA AATGACAGAT CTCTGCTTTG GAAATCACAC GTCTGGCTTC	1211
Ala	
ACAGATGTGT GATTACAGT GTGAATCTTG GTGTCTACGT TACCAGGCAG GAAGGCTGAG	1271
AGGAGAGAGA CTCCAGCTGG GTTGGA AAC AGTATTTTCC AAACCTACCTT CCAGTTCCTC	1331
ATTTTTGAAT ACAGGCATAG AGTTCAGACT TTTTTTAAAT AGTAAAAATA AAATTAAAGC	1391
TGAAAACTGC AACTTGTAAG TGTGGTAAAG AGTTAGTTTG AGTTGCTATC ATGTCAAACG	1451
TGAAAATGCT GTATTAGTCA CAGAGATAAT TCTAGCTTTG AGCTTAAGAA TTTTGAGCAG	1511
GTGGTATGTT TGGGAGACTG CTGAGTCAAC CCAATAGTTG TTGATTGGCA GGAGTTGGAA	1571
GTGTGTGATC TGTGGGCACA TTAGCCTATG TGCATGCAGC ATCTAAGTAA TGATGTCGTT	1631
TGAATCACAG TATACGCTCC ATCGCTGTCA TCTCAGCTGG ATCTCCATTC TCTCAGGCTT	1691
GCTGCCAAAA GCCTTTTGTG TTTTGTTTTG TATCATTATG AAGTCATGCG TTTAATCACA	1751
TTCGAGTGTT TCAGTGCTTC GCAGATGTCC TTGATGCTCA TATTGTTCCC TAATTTGCCA	1811
GTGGGAACTC CTAAATCAAA TTGGCTTCTA ATCAAAGCTT TTAAACCCTA TTGGTAAAGA	1871
ATGGAAGGTG GAGAAGCTCC CTGAAGTAAG CAAAGACTTT CCTCTTAGTC GAGCCAAGTT	1931
AAGAATGTTT TTATGTTGCC CAGTGTGTTT CTGATCTGAT GCAAGCAAGA AACACTGGGC	1991
TTCTAGAACC AGGCAACTTG GGAAC TAGAC TCCCAAGCTG GACTATGGCT CTACTTTCAG	2051

GCCACATGGC TAAAGAAGGT TTCAGAAAGA AGTGGGGACA GAGCAGAACT TTCACCTTCA 2111
TATATTTGTA TGATCCTAAT GAATGCATAA AATGTTAAGT TGATGGTGAT GAAATGTAAA 2171
TACTGTTTTT AACAACTATG ATTTGGAAAA TAAATCAATG CTATAACTAT GTTGATAAAA 2231
G 2232

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Leu Ser Thr Ser Arg Ser Arg Phe Ile Arg Asn Thr Asn Glu Ser
1 5 10 15
Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
20 25 30
His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
35 40 45
Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
50 55 60
Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
65 70 75 80
Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
85 90 95
Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
100 105 110
Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
115 120 125
Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
130 135 140
Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
145 150 155 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 165 170 175
 Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 180 185 190
 Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 195 200 205
 Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220
 Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240
 Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255
 Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270
 Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 275 280 285
 Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300
 Tyr Ala Phe Val Gly Glu Lys Phe Arg Ser Leu Phe His Ile Ala Leu
 305 310 315 320
 Gly Cys Arg Ile Ala Pro Leu Gln Lys Pro Val Cys Gly Gly Pro Gly
 325 330 335
 Val Arg Pro Gly Lys Asn Val Lys Val Thr Thr Gln Gly Leu Leu Asp
 340 345 350
 Gly Arg Gly Lys Gly Lys Ser Ile Gly Arg Ala Pro Glu Ala Ser Leu
 355 360 365
 Gln Asp Lys Glu Gly Ala
 370

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1979 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
- (A) NAME/KEY: CDS
- (B) LOCATION: 81..1160
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGGACTGCC TGAGACAAGC CACAAGCTGA ACAGAGAAAG TGGATTGAAC AAGGACGCAT	60
TTCCCCAGTA CATCCACAAC ATG CTG TCC ACA TCT CGT TCT CGG TTT ATC	110
Met Leu Ser Thr Ser Arg Ser Arg Phe Ile	
1 5 10	
AGA AAT ACC AAC GAG AGC GGT GAA GAA GTC ACC ACC TTT TTT GAT TAT	158
Arg Asn Thr Asn Glu Ser Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr	
15 20 25	
GAT TAC GGT GCT CCC TGT CAT AAA TTT GAC GTG AAG CAA ATT GGG GCC	206
Asp Tyr Gly Ala Pro Cys His Lys Phe Asp Val Lys Gln Ile Gly Ala	
30 35 40	
CAA CTC CTG CCT CCG CTC TAC TCG CTG GTG TTC ATC TTT GGT TTT GTG	254
Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val	
45 50 55	
GGC AAC ATG CTG GTC GTC CTC ATC TTA ATA AAC TGC AAA AAG CTG AAG	302
Gly Asn Met Leu Val Val Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys	
60 65 70	
TGC TTG ACT GAC ATT TAC CTG CTC AAC CTG GCC ATC TCT GAT CTG CTT	350
Cys Leu Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu	
75 80 85 90	
TTT CTT ATT ACT CTC CCA TTG TGG GCT CAC TCT GCT GCA AAT GAG TGG	398
Phe Leu Ile Thr Leu Pro Leu Trp Ala His Ser Ala Ala Asn Glu Trp	
95 100 105	
GTC TTT GGG AAT GCA ATG TGC AAA TTA TTC ACA GGG CTG TAT CAC ATC	446
Val Phe Gly Asn Ala Met Cys Lys Leu Phe Thr Gly Leu Tyr His Ile	
110 115 120	
GGT TAT TTT GGC GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGA	494
Gly Tyr Phe Gly Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg	
125 130 135	

TAC CTG GCT ATT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC	542
Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val	
140 145 150	
ACC TTT GGG GTG GTG ACA AGT GTG ATC ACC TGG TTG GTG GCT GTG TTT	590
Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp Leu Val Ala Val Phe	
155 160 165 170	
GCT TCT GTC CCA GGA ATC ATC TTT ACT AAA TGC CAG AAA GAA GAT TCT	638
Ala Ser Val Pro Gly Ile Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser	
175 180 185	
GTT TAT GTC TGT GGC CCT TAT TTT CCA CGA GGA TGG AAT AAT TTC CAC	686
Val Tyr Val Cys Gly Pro Tyr Phe Pro Arg Gly Trp Asn Asn Phe His	
190 195 200	
ACA ATA ATG AGG AAC ATT TTG GGG CTG GTC CTG CCG CTG CTC ATC ATG	734
Thr Ile Met Arg Asn Ile Leu Gly Leu Val Leu Pro Leu Leu Ile Met	
205 210 215	
GTC ATC TGC TAC TCG GGA ATC CTG AAA ACC CTG CTT CGG TGT CGA AAC	782
Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn	
220 225 230	
GAG AAG AAG AGG CAT AGG GCA GTG AGA GTC ATC TTC ACC ATC ATG ATT	830
Glu Lys Lys Arg His Arg Ala Val Arg Val Ile Phe Thr Ile Met Ile	
235 240 245 250	
GTT TAC TTT CTC TTC TGG ACT CCC TAT AAC ATT GTC ATT CTC CTG AAC	878
Val Tyr Phe Leu Phe Trp Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn	
255 260 265	
ACC TTC CAG GAA TTC TTC GGC CTG AGT AAC TGT GAA AGC ACC AGT CAA	926
Thr Phe Gln Glu Phe Phe Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln	
270 275 280	
CTG GAC CAA GCC ACG CAG GTG ACA GAG ACT CTT GGG ATG ACT CAC TGC	974
Leu Asp Gln Ala Thr Gln Val Thr Glu Thr Leu Gly Met Thr His Cys	
285 290 295	
TGC ATC AAT CCC ATC ATC TAT GCC TTC GTT GGG GAG AAG TTC AGA AGG	1022
Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg	
300 305 310	
TAT CTC TCG GTG TTC TTC CGA AAG CAC ATC ACC AAG CGC TTC TGC AAA	1070
Tyr Leu Ser Val Phe Phe Arg Lys His Ile Thr Lys Arg Phe Cys Lys	
315 320 325 330	

CAA TGT CCA GTT TTC TAC AGG GAG ACA GTG GAT GGA GTG ACT TCA ACA	1118
Gln Cys Pro Val Phe Tyr Arg Glu Thr Val Asp Gly Val Thr Ser Thr	
335 340 345	
AAC ACG CCT TCC ACT GGG GAG CAG GAA GTC TCG GCT GGT TTA	1160
Asn Thr Pro Ser Thr Gly Glu Gln Glu Val Ser Ala Gly Leu	
350 355 360	
TAAAACGAGG AGCAGTTTGA TTGTTGTTTA TAAAGGGAGA TAACAATCTG TATATAACAA	1220
CAAACCTTCAA GGGTTTGTTG AACAATAGAA ACCTGTAAAG CAGGTGCCCA GGAACCTCAG	1280
GGCTGTGTGT ACTAATACAG ACTATGTCAC CCAATGCATA TCCAACATGT GCTCAGGGAA	1340
TAATCCAGAA AAACGTGTTGG TAGAGACTTT GACTCTCCAG AAAGCTCATC TCAGCTCCTG	1400
AAAAATGCCT CATTACCTTG TGCTAATCCT CTTTTTCTAG TCTTCATAAT TTCTTCACTC	1460
AATCTCTGAT TCTGTCAATG TCTTGAAATC AAGGGCCAGC TGGAGGTGAA GAAGAGAATG	1520
TGACAGGCAC AGATGAATGG GAGTGAGGGA TAGTGGGGTC AGGGCTGAGA GGAGAAGGAG	1580
GGAGACATGA GCATGGCTGA GCCTGGACAA AGACAAAGGT GAGCAAAGGG CTCACGCATT	1640
CAGCCAGGAG ATGATACTGG TCCTTAGCCC CATCTGCCAC GTGTATTAA CTTGAAGGG	1700
TTCACCAGGT CAGGGAGAGT TTGGGAACTG CAATAACCTG GGAGTTTTGG TGGAGTCCGA	1760
TGATTCTCTT TTGCATAAGT GCATGACATA TTTTGTCTTT ATTACAGTTT ATCTATGGCA	1820
CCCATGCACC TTACATTTGA AATCTATGAA ATATCATGCT CCATTGTTCA GATGCTTCTT	1880
AGGCCACATC CCCCTGTCTA AAAATTCAGA AAATTTTGT TTATAAAGA TGCATTATCT	1940
ATGATATGCT AATATATGTA TATGCAATAT AAAATTTAG	1979

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Leu	Ser	Thr	Ser	Arg	Ser	Arg	Phe	Ile	Arg	Asn	Thr	Asn	Glu	Ser
1				5					10					15	

Gly Glu Glu Val Thr Thr Phe Phe Asp Tyr Asp Tyr Gly Ala Pro Cys
 20 25 30

His Lys Phe Asp Val Lys Gln Ile Gly Ala Gln Leu Leu Pro Pro Leu
 35 40 45

Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn Met Leu Val Val
 50 55 60

Leu Ile Leu Ile Asn Cys Lys Lys Leu Lys Cys Leu Thr Asp Ile Tyr
 65 70 75 80

Leu Leu Asn Leu Ala Ile Ser Asp Leu Leu Phe Leu Ile Thr Leu Pro
 85 90 95

Leu Trp Ala His Ser Ala Ala Asn Glu Trp Val Phe Gly Asn Ala Met
 100 105 110

Cys Lys Leu Phe Thr Gly Leu Tyr His Ile Gly Tyr Phe Gly Gly Ile
 115 120 125

Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val His
 130 135 140

Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr
 145 150 155 160

Ser Val Ile Thr Trp Leu Val Ala Val Phe Ala Ser Val Pro Gly Ile
 165 170 175

Ile Phe Thr Lys Cys Gln Lys Glu Asp Ser Val Tyr Val Cys Gly Pro
 180 185 190

Tyr Phe Pro Arg Gly Trp Asn Asn Phe His Thr Ile Met Arg Asn Ile
 195 200 205

Leu Gly Leu Val Leu Pro Leu Leu Ile Met Val Ile Cys Tyr Ser Gly
 210 215 220

Ile Leu Lys Thr Leu Leu Arg Cys Arg Asn Glu Lys Lys Arg His Arg
 225 230 235 240

Ala Val Arg Val Ile Phe Thr Ile Met Ile Val Tyr Phe Leu Phe Trp
 245 250 255

Thr Pro Tyr Asn Ile Val Ile Leu Leu Asn Thr Phe Gln Glu Phe Phe
 260 265 270

Gly Leu Ser Asn Cys Glu Ser Thr Ser Gln Leu Asp Gln Ala Thr Gln
 275 280 285

Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile Asn Pro Ile Ile
 290 295 300

Tyr Ala Phe Val Gly Glu Lys Phe Arg Arg Tyr Leu Ser Val Phe Phe
 305 310 315 320

Arg Lys His Ile Thr Lys Arg Phe Cys Lys Gln Cys Pro Val Phe Tyr
 325 330 335

Arg Glu Thr Val Asp Gly Val Thr Ser Thr Asn Thr Pro Ser Thr Gly
 340 345 350

Glu Gln Glu Val Ser Ala Gly Leu
 355 360

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Glu Thr Pro Asn Thr Thr Glu Asp Tyr Asp Thr Thr Thr Glu Phe
 1 5 10 15

Asp Tyr Gly Asp Ala Thr Pro Cys Gln Lys Val Asn Glu Arg Ala Phe
 20 25 30

Gly Ala Gln Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe Val Ile Gly
 35 40 45

Leu Val Gly Asn Ile Leu Val Val Leu Val Leu Val Gln Tyr Lys Arg
 50 55 60

Leu Lys Asn Met Thr Ser Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
 65 70 75 80

Leu Leu Phe Leu Phe Thr Leu Pro Phe Trp Ile Asp Tyr Lys Leu Lys
 85 90 95

Asp	Asp	Trp	Val	Phe	Gly	Asp	Ala	Met	Cys	Lys	Ile	Leu	Ser	Gly	Phe	100	105	110	
Tyr	Tyr	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	115	120	125	
Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Leu	Arg	Ala	130	135	140	
Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Ile	Ile	Trp	Ala	Leu	145	150	155	160
Ala	Ile	Leu	Ala	Ser	Met	Pro	Gly	Leu	Tyr	Phe	Ser	Lys	Thr	Gln	Trp	165	170	175	
Glu	Phe	Thr	His	His	Thr	Cys	Ser	Leu	His	Phe	Pro	His	Glu	Ser	Leu	180	185	190	
Arg	Glu	Trp	Lys	Leu	Phe	Gln	Ala	Leu	Lys	Leu	Asn	Leu	Phe	Gly	Leu	195	200	205	
Val	Leu	Pro	Leu	Leu	Val	Met	Ile	Ile	Cys	Tyr	Thr	Gly	Ile	Ile	Lys	210	215	220	
Ile	Leu	Leu	Arg	Arg	Pro	Asn	Glu	Lys	Lys	Ser	Lys	Ala	Val	Arg	Leu	225	230	235	240
Ile	Phe	Val	Ile	Met	Ile	Ile	Phe	Phe	Leu	Phe	Trp	Thr	Pro	Tyr	Asn	245	250	255	
Leu	Thr	Ile	Leu	Ile	Ser	Val	Phe	Gln	Asp	Phe	Leu	Phe	Thr	His	Glu	260	265	270	
Cys	Glu	Gln	Ser	Arg	His	Leu	Asp	Leu	Ala	Val	Gln	Val	Thr	Glu	Val	275	280	285	
Ile	Ala	Tyr	Thr	His	Cys	Cys	Val	Asn	Pro	Val	Ile	Tyr	Ala	Phe	Val	290	295	300	
Gly	Glu	Arg	Phe	Arg	Lys	Tyr	Leu	Arg	Gln	Leu	Phe	His	Arg	Arg	Val	305	310	315	320
Ala	Val	His	Leu	Val	Lys	Trp	Leu	Pro	Phe	Leu	Ser	Val	Asp	Arg	Leu	325	330	335	
Glu	Arg	Val	Ser	Ser	Thr	Ser	Pro	Ser	Thr	Gly	Glu	His	Glu	Leu	Ser	340	345	350	
Ala	Gly	Phe														355			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gly Ile Ser Ile Tyr Thr Ser Asp Asn Tyr Thr Glu Glu Met
1 5 10 15

Gly Ser Gly Asp Tyr Asp Ser Met Lys Glu Pro Cys Phe Arg Glu Glu
20 25 30

Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Tyr Ile Tyr Ser Ile Ile
35 40 45

Phe Leu Tyr Gly Ile Val Gly Asn Gly Leu Val Ile Leu Val Met Gly
50 55 60

Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys Tyr Arg Leu His Leu
65 70 75 80

Ser Val Ala Asp Leu Leu Phe Val Ile Thr Leu Pro Phe Trp Ala Val
85 90 95

Asp Ala Val Ala Asn Trp Tyr Phe Gly Asn Phe Leu Cys Lys Ala Val
100 105 110

His Val Ile Tyr Thr Val Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala
115 120 125

Phe Ile Ser Leu Asp Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser
130 135 140

Gln Arg Pro Arg Lys Leu Leu Ala Glu Lys Val Val Tyr Val Gly Val
145 150 155 160

Trp Ile Pro Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn
165 170 175

Val Ser Glu Ala Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn
 180 185 190
 Asp Leu Trp Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu
 195 200 205
 Ile Leu Pro Gly Ile Val Ile Leu Phe Cys Tyr Cys Ile Ile Ile Ser
 210 215 220
 Lys Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Tyr
 225 230 235 240
 Tyr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr Tyr
 245 250 255
 Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile Lys Gln
 260 265 270
 Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser Ile Thr Glu
 275 280 285
 Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe
 290 295 300
 Leu Gly Ala Lys Phe Lys Tyr Ser Ala Gln His Ala Leu Thr Ser Val
 305 310 315 320
 Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly
 325 330 335
 His Ser Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
 340 345 350

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Asn	Ile	Thr	Asp	Pro	Gln	Met	Trp	Asp	Phe	Asp	Asp	Leu	Asn	1	5	10	15
Phe	Thr	Gly	Met	Pro	Pro	Ala	Asp	Glu	Asp	Tyr	Ser	Pro	Cys	Met	Leu	20	25	30	
Glu	Thr	Glu	Thr	Leu	Asn	Lys	Tyr	Val	Val	Ile	Ile	Ala	Tyr	Ala	Leu	35	40	45	
Val	Phe	Leu	Leu	Ser	Leu	Leu	Gly	Asn	Ser	Leu	Val	Met	Leu	Val	Ile	50	55	60	
Leu	Tyr	Ser	Arg	Val	Gly	Arg	Ser	Val	Thr	Asp	Val	Tyr	Leu	Leu	Asn	65	70	75	80
Leu	Ala	Leu	Ala	Asp	Leu	Leu	Phe	Ala	Leu	Thr	Leu	Pro	Ile	Trp	Ala	85	90	95	
Ala	Ser	Lys	Val	Asn	Gly	Trp	Ile	Phe	Gly	Thr	Phe	Leu	Cys	Lys	Val	100	105	110	
Val	Ser	Leu	Leu	Lys	Glu	Val	Asn	Phe	Tyr	Ser	Gly	Ile	Leu	Leu	Leu	115	120	125	
Ala	Cys	Ile	Ser	Val	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Thr	Arg	130	135	140	
Thr	Leu	Thr	Gln	Lys	Arg	His	Leu	Val	Lys	Phe	Val	Cys	Leu	Gly	Cys	145	150	155	160
Trp	Gly	Leu	Ser	Met	Asn	Leu	Ser	Leu	Pro	Phe	Phe	Leu	Phe	Arg	Gln	165	170	175	
Ala	Tyr	His	Pro	Asn	Asn	Ser	Ser	Pro	Val	Cys	Tyr	Glu	Val	Leu	Gly	180	185	190	
Asn	Asp	Thr	Ala	Lys	Trp	Arg	Met	Val	Leu	Arg	Ile	Leu	Pro	His	Thr	195	200	205	
Phe	Gly	Phe	Ile	Val	Pro	Leu	Phe	Val	Met	Leu	Phe	Cys	Tyr	Gly	Phe	210	215	220	
Thr	Leu	Arg	Thr	Leu	Phe	Lys	Ala	His	Met	Gly	Gln	Lys	His	Arg	Ala	225	230	235	240
Met	Arg	Val	Ile	Phe	Ala	Val	Val	Leu	Ile	Phe	Leu	Leu	Cys	Trp	Leu	245	250	255	
Pro	Tyr	Asn	Leu	Val	Leu	Leu	Ala	Asp	Thr	Leu	Met	Arg	Thr	Gln	Val	260	265	270	

Ile Gln Glu Thr Cys Glu Arg Arg Asn Asn Ile Gly Arg Ala Leu Asp
 275 280 285
 Ala Thr Glu Ile Leu Gly Phe Leu His Ser Cys Leu Asn Pro Ile Ile
 290 295 300
 Tyr Ala Phe Ile Gly Gln Asn Phe Arg His Gly Phe Leu Lys Ile Leu
 305 310 315 320
 Ala Met His Gly Leu Val Ser Lys Glu Phe Leu Ala Arg His Arg Val
 325 330 335
 Thr Ser Tyr Thr Ser Ser Ser Val Asn Val Ser Ser Asn Leu
 340 345 350

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Ser Asp Ser Phe Glu Asp Phe Trp Lys Gly Glu Asp Leu Ser
 1 5 10 15
 Asn Tyr Ser Tyr Ser Ser Thr Leu Pro Pro Phe Leu Leu Asp Ala Ala
 20 25 30
 Pro Cys Glu Pro Glu Ser Leu Glu Ile Asn Lys Tyr Phe Val Val Ile
 35 40 45
 Ile Tyr Ala Leu Val Phe Leu Leu Ser Leu Leu Gly Asn Ser Leu Val
 50 55 60
 Met Leu Val Ile Leu Tyr Ser Arg Val Gly Arg Ser Val Thr Asp Val
 65 70 75 80
 Tyr Leu Leu Asn Leu Ala Leu Ala Asp Leu Leu Phe Ala Leu Thr Leu
 85 90 95
 Pro Ile Trp Ala Ala Ser Lys Val Asn Gly Trp Ile Phe Gly Thr Phe
 100 105 110

Leu Cys Lys Val Val Ser Leu Leu Lys Glu Val Asn Phe Tyr Ser Gly
 115 120 125
 Ile Leu Leu Leu Ala Cys Ile Ser Val Asp Arg Tyr Leu Ala Ile Val
 130 135 140
 His Ala Thr Arg Thr Leu Thr Gln Lys Arg Tyr Leu Val Lys Phe Ile
 145 150 155 160
 Cys Leu Ser Ile Trp Gly Leu Ser Leu Leu Leu Ala Leu Pro Val Leu
 165 170 175
 Leu Phe Arg Arg Thr Val Tyr Ser Ser Asn Val Ser Pro Ala Cys Tyr
 180 185 190
 Glu Asp Met Gly Asn Asn Thr Ala Asn Trp Arg Met Leu Leu Arg Ile
 195 200 205
 Leu Pro Gln Ser Phe Gly Phe Ile Val Pro Leu Leu Ile Met Leu Phe
 210 215 220
 Cys Tyr Gly Phe Thr Leu Arg Thr Leu Phe Lys Ala His Met Gly Gln
 225 230 235 240
 Lys His Arg Ala Met Arg Val Ile Phe Ala Val Val Leu Ile Phe Leu
 245 250 255
 Leu Cys Trp Leu Pro Tyr Asn Leu Val Leu Leu Ala Asp Thr Leu Met
 260 265 270
 Arg Thr Gln Val Ile Gln Glu Thr Cys Glu Arg Arg Asn His Ile Asp
 275 280 285
 Arg Ala Leu Asp Ala Thr Glu Ile Leu Gly Ile Leu His Ser Cys Leu
 290 295 300
 Asn Pro Leu Ile Tyr Ala Phe Ile Gly Gln Lys Phe Arg His Gly Leu
 305 310 315 320
 Leu Lys Ile Leu Ala Ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro
 325 330 335
 Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser
 340 345 350
 Thr Thr Leu
 355

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGCTCGAGAC CTRKCMDTKK CYGACCT

27

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCGAATTCTG GACRATGGCC AGGTAVCKGT C

31

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asn Leu Ala Ile Ser Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Asp Arg Tyr Leu Ala Ile Val
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val
1 5 10 15

His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe Gly Val
20 25 30

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu Ala Ile Val
1 5 10 15

His Ala Val Phe Ala Leu Arg Ala Arg Thr Val Thr Phe Gly Val
20 25 30